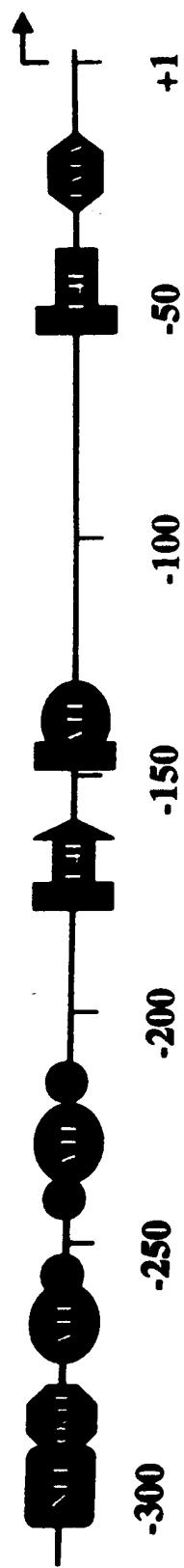


FIGURE 1

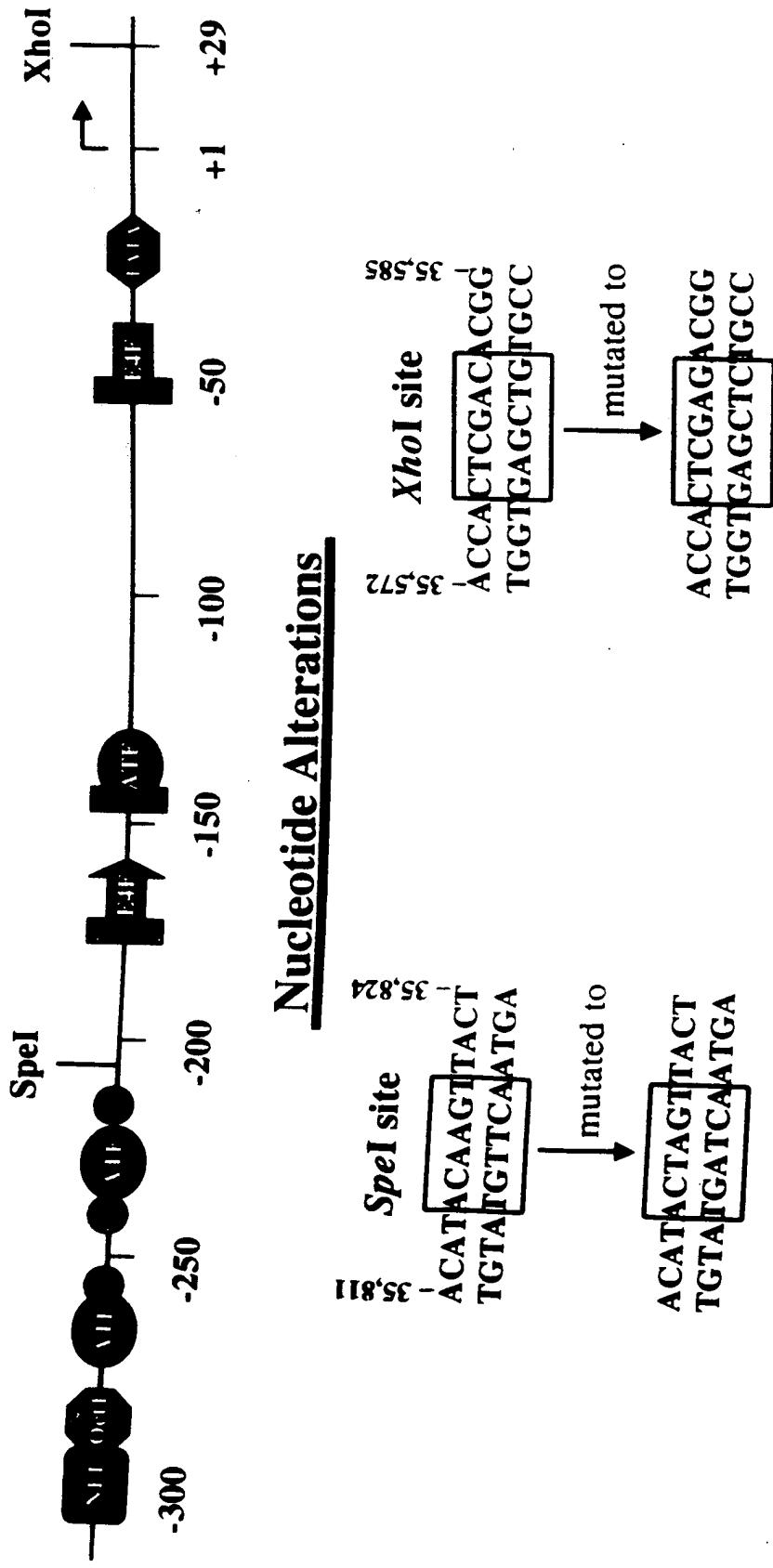


### Symbol Legend:

- NF-I binding site centered around -300
- Oct1 binding site positioned near -285
- ATF binding sites near -260, -230, and -140
- Sp1 binding sites near -255, -240, and -220
- E4F inverted repeat binding sites near -165 and -50
- E4TF1 binding site positioned around -140
- TATA box positioned near -30
- transcriptional start site denoted as +1

FIGURE 2

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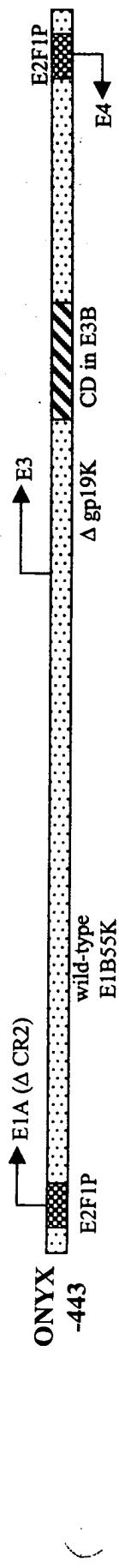


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FIGURE 3

Figure 4.

A.



B.

ONYX 443

0 12 24 36 48 60 72

C33-A  
H1299  
DU145  
LNCaP

0 12 24 36 48 72

Hepatocytes

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Figure 5.

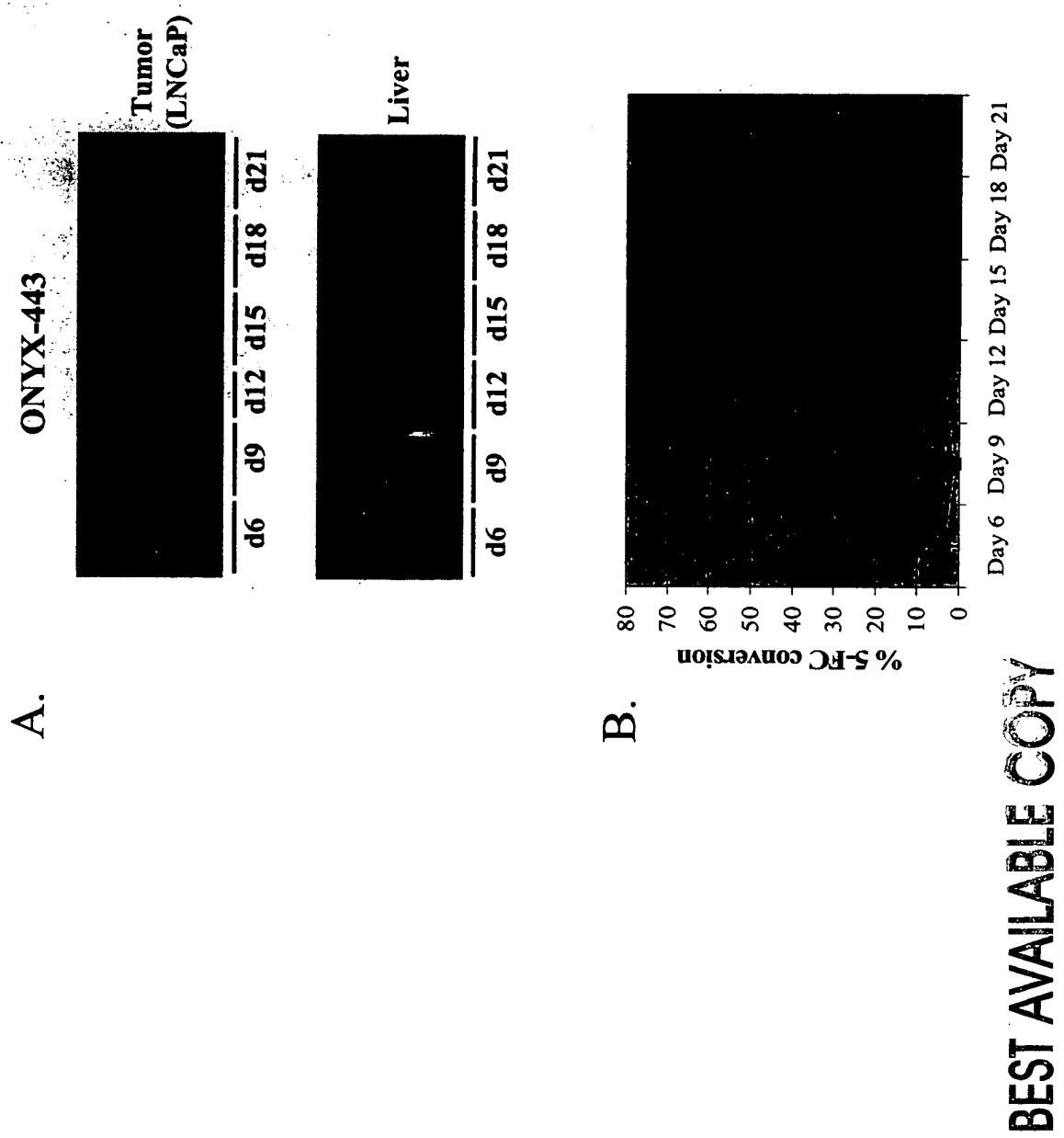
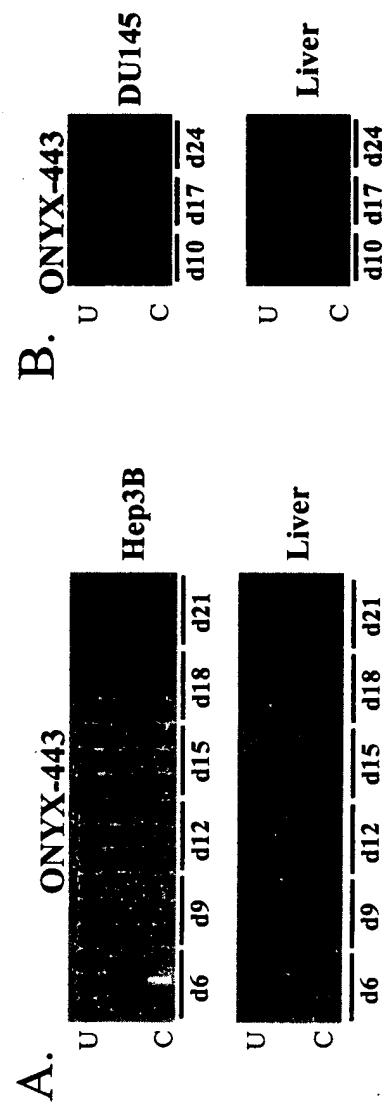


Figure 6.



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Figure 1. Genomic changes in ONYX-4XXX. ITR: inverted terminal repeat;  $\psi$ : Viral packaging sequence; E2F1P: E2F1 promoter; H: Hind III site; B: BamH I site; X: Xho I site; S: Spe I site.

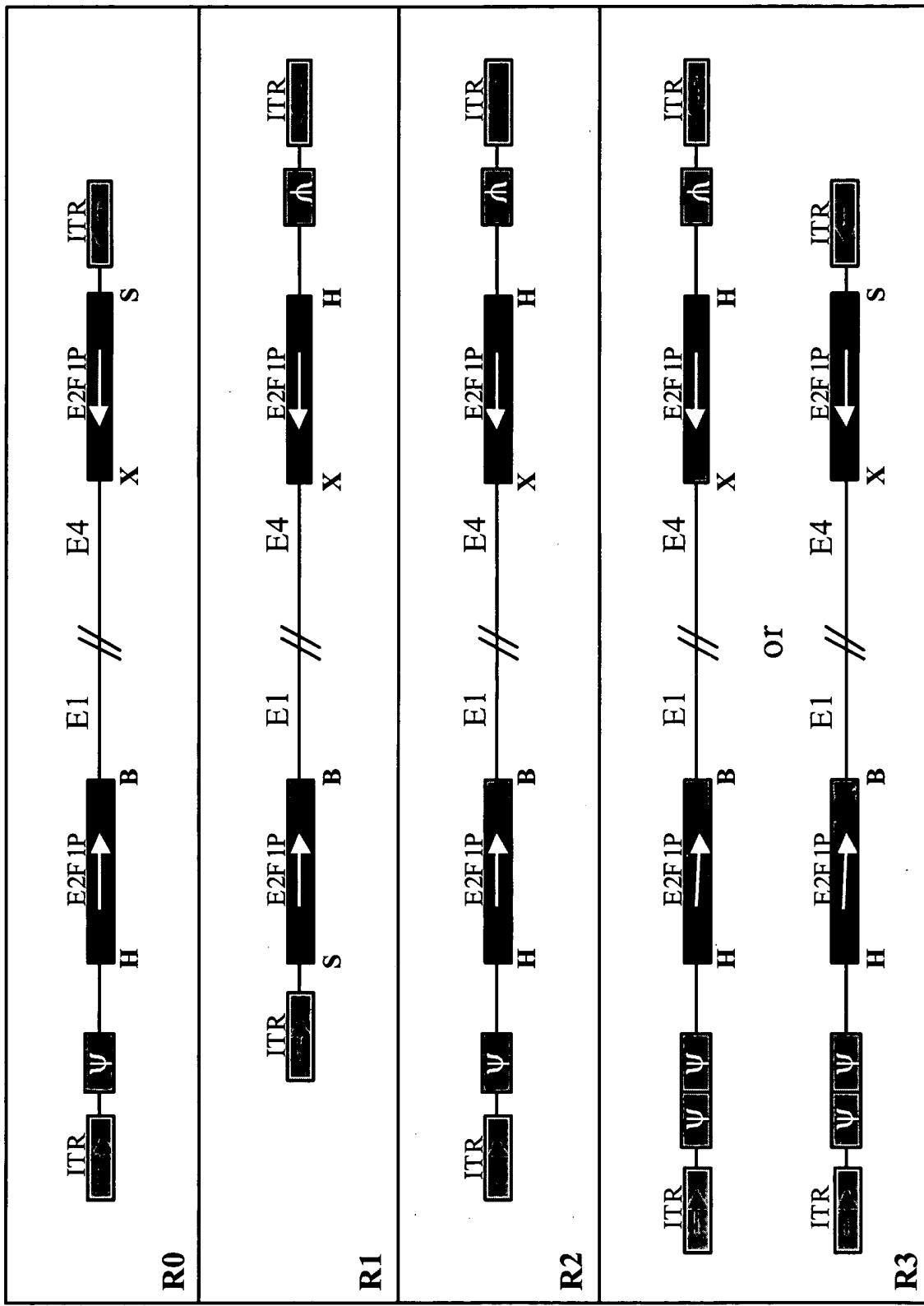
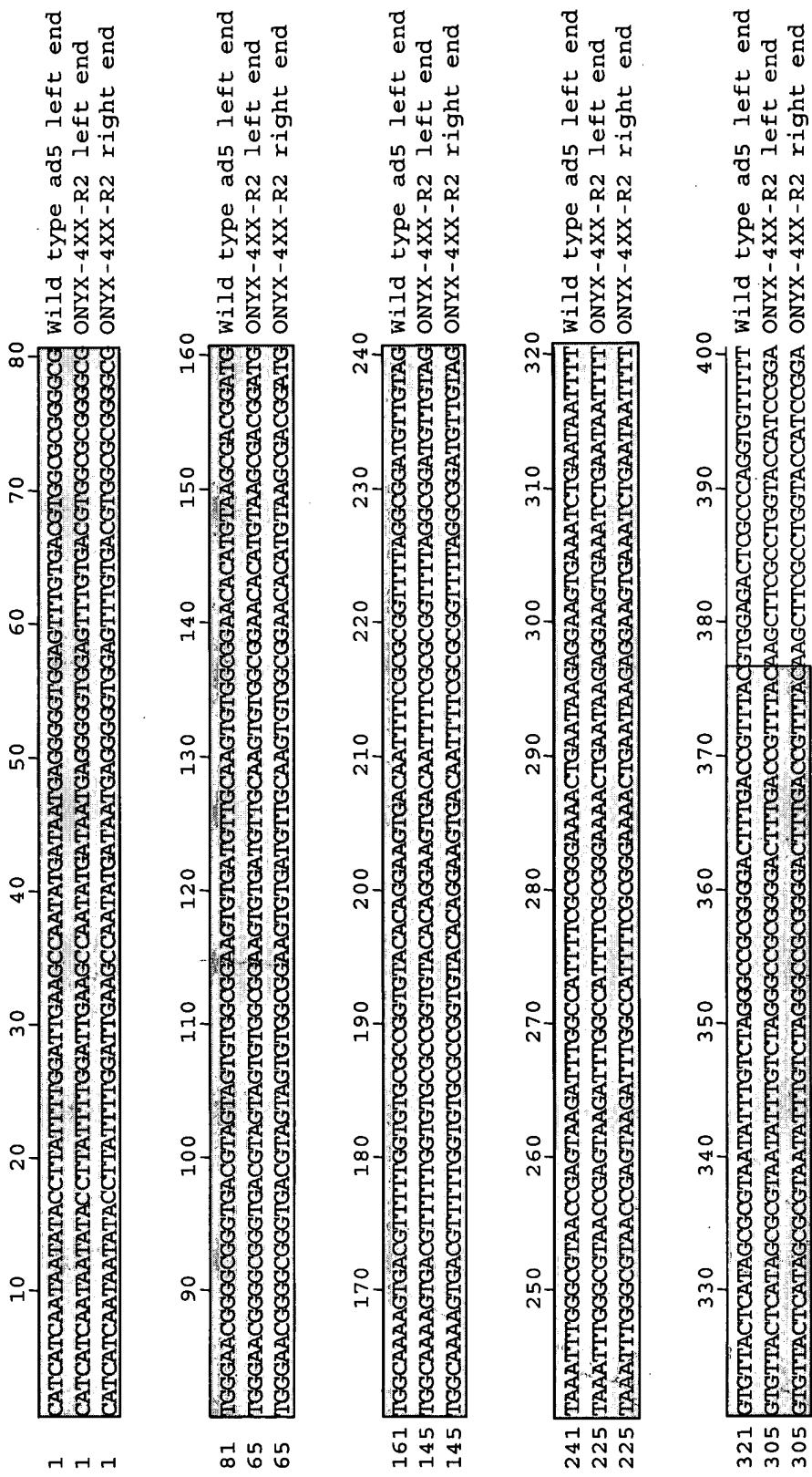
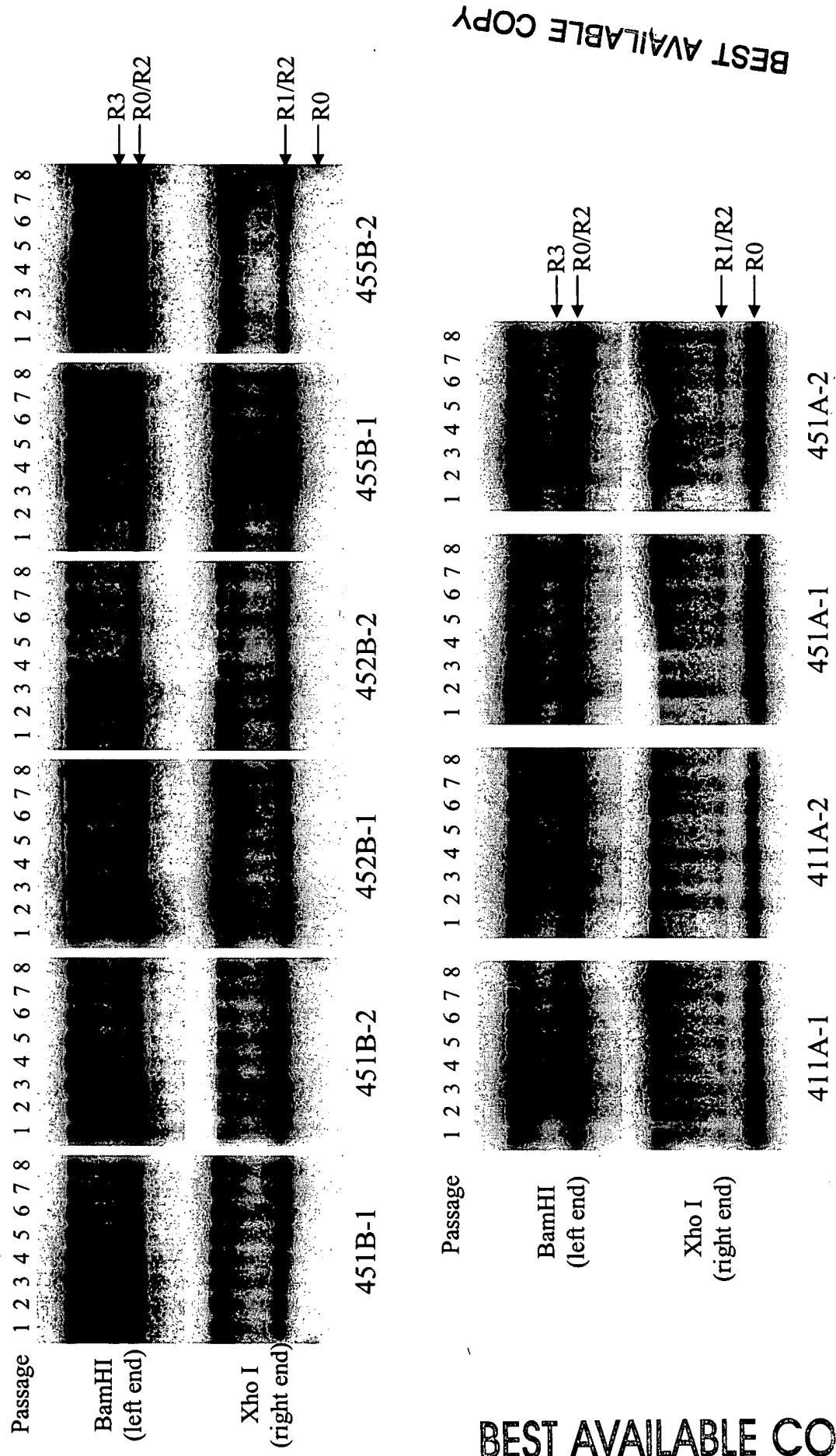


Figure 8. Sequencing Confirmation of ONYX-4XX R2 Termini



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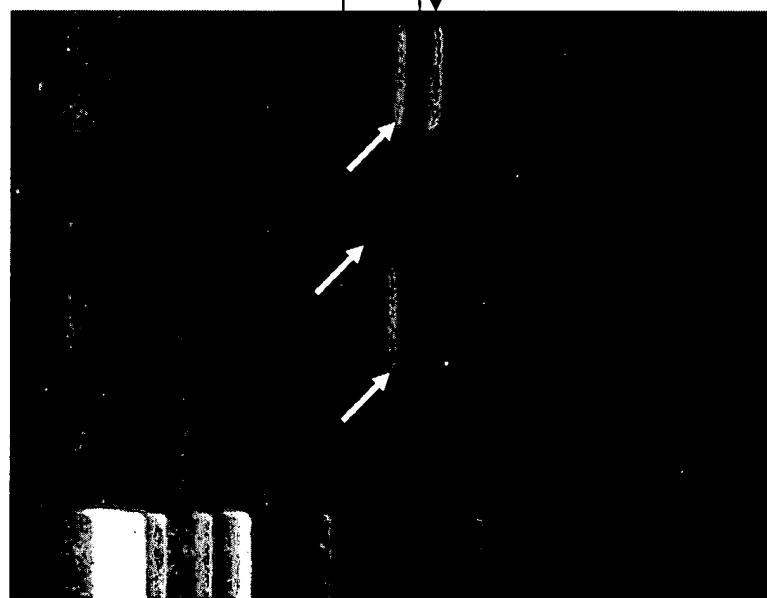
Figure 9 Southern Analysis of Viruses from Serial Passaging



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Figure 10. PCR Analysis of New Species

411A (4110 packaging)  
451B (451D)<sup>-1</sup>  
455B (455F)<sup>-2</sup>



PCR with P3/P5.

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Figure 11. Duplication of Packaging Sequence

1 -GTGTTAGTAATTTGGG 107 bp YCD1 . SEQ  
1 -TGTGTTAGTAATTTGGG 115 bp TNF2 . SEQ  
1 -GAGTTTGGTGCACGGGTACAGGAAGTGACAATTTCGCGGGTTAGGCCATGTTAGTAATTTGGG 202 bp TNF1 . SEQ  
1 -GGTGTACACGGAACTCAATTTCGCGGGTTAGGGCATGTTAGGGATGTTGTCATAAATTTGGG Ad5 packaging seq

AI

18 CGTAACCCAGTAAGATTTGGCCATTTCGCGGGAAACTGAAATAAGGCCAACGICAATAATTTCGTTGTTACTCA 107 bp YCD1 . SEQ  
19 CGTAACCCAGTAAGATTTGGCCATTTCGCGGGAAACTGAAATAAGGCCAACGICAATAATTTCGTTGTTACTCA 115 bp TNF2 . SEQ  
81 CGTAACCCAGTAAGATTTGGCCATTTCGCGGGAAACTGAAATAAGGCCAACGICAATAATTTCGTTGTTACTCA 202 bp TNF1 . SEQ  
62 CGTAACCCAGTAAGATTTGGCCATTTCGCGGGAAACTGAAATAAGGCCAACGICAATAATTTCGTTGTTACTCA Ad5 packaging seq

AII

AIII AIV

98 TAGGCCCTAA  
99 TAGGCCGTAAATTGTT  
161 TAGGCCGTAAATTGTTGCTAGCCCCCGGCGCTGACCTTGACCGT  
142 TAGGCCGTAAATTGCTAGCCCCCGGCGCTGACCTTGACCGT

AV AVI AVII

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